AMENDMENTS TO THE SPECIFICATION:

Please amend the paragraph on page 28, lines 24-29, to page 29, lines 1-4, as follows:

Nucleic acids coding for a protein exhibiting alpha-1,4-glucan-phosphorylating enzymatic activity can be identified, for example, by scrutinising databases such as those made available, for example by EMBL (~~http://~~www.ebi.ac.uk/Tools/index.htm) or NCBI (National Center for Biotechnology Information, ~~http://~~www.ncbi.nlm.nih.gov/). In this case one or a plurality of amino acid sequences determined when implementing the method according to the invention, is pre-defined as a so-called query. This query sequence is then compared by means of statistical computer programs with sequences, which are contained in the selected databases. Such database queries (e.g. blast or fasta searches) are known to the person skilled in the art and can be carried out by various providers.

Please amend the paragraph on page 29, lines 6-11, as follows:

If such a database query is carried out, e.g. at the NCBI (National Center for Biotechnology Information, ~~http://~~www.ncbi.nlm.nih.gov/), then the standard settings, which are specified for the particular comparison inquiry, should be used. For protein sequence comparisons (blastp), these are the following settings: Limit entrez = not activated; Filter = low complexity activated; Expect value = 10; word size = 3; Matrix = BLOSUM62; Gap costs: Existence = 11, Extension = 1.

Please amend the paragraph on page 61, lines 22-30, to page 62, lines 1-16, as follows:

b) Identification of proteins, which have increased binding activity towards P-starch in comparison with non-phosphorylated starch

Proteins identified in accordance with Step a) are digested with trypsin and the peptides obtained are analysed by means of MALDI-TOF to determine the masses of the peptides obtained. Trypsin is a sequence-specific protease, i.e. trypsin only splits proteins at a specified position when the proteins concerned contain certain amino acid sequences. Trypsin always splits peptide bonds when the amino acids arginine and lysine follow one another starting from the N-terminus. In this way, it is possible to theoretically determine all peptides that would be produced following the trypsin digestion of an amino acid sequence. From the knowledge of the amino acids coding for the theoretically determined peptides, the masses of the peptides, which are obtained after theoretical trypsin digestion, can also be determined. Databases (e.g. NCBInr ~~http://~~prospector.ucsf.edu/ucsfhtml4.0/msfit.htm; Swissprot ~~http://~~cbrg. inf.ethz.ch/Server/MassSearch.html), which contain information concerning the masses of peptides

after theoretical trypsin digestion, can therefore be compared with the real masses of peptides of unknown proteins obtained with MALDI-TOF-MS. Amino acid sequences, which have the same peptide masses after theoretical and/or real trypsin digestion, are to be looked upon as being identical. The databases concerned contain both peptide masses of proteins, the function of which has already been shown, and also peptide masses of proteins, which up to now only exist hypothetically by derivation from amino acid sequences starting from nucleic acid sequences obtained in sequencing projects. The actual existence and the function of such hypothetical proteins has therefore seldom been shown and, if there is a function at all, then this is usually based only on predictions and not on an actual demonstration of the function.

Please amend the paragraph on page 76, lines 1-24, as follows:

The band of the protein with a molecular weight of ca. 130 kDa identified in Step e) was excised from the gel. The protein was subsequently released from the acrylamide as described under General Methods 10 b), digested with trypsin and the peptide masses obtained determined by means of MALDI-TOF-MS. The so-called "fingerprint" obtained by MALDI-TOF-MS was compared with fingerprints of theoretically digested amino acid molecules in databases (Mascot: ~~http://~~www.matrixscience.com/search_form_select.html; ProFound: ~~http://~~129.85.19.192/profound_bin/WebProFound.exe; PepSea: ~~http://~~195.41.108.38/PepSeaIntro.html). As such a fingerprint is very specific to a protein, it was possible to identify an amino acid molecule. Using the sequence of this amino acid molecule, it was possible to isolate a nucleic acid sequence from Arabidopsis thaliana coding for an OK1 protein. The protein identified using this method was designated as A.t.-OK1. After analysing the amino acid sequence from Arabidopsis thaliana, it was found that this deviates from the sequence present in the database (NP 198009, NCBI). The amino acid sequence shown in SEQ ID No 2 codes for the A.t.-OK1 protein. SEQ ID No 2 contains deviations when compared with the sequence in the database (Acc.: NP 198009.1, NCBI). The amino acids 519 to 523 (WRLCE) and 762 to 766 (VRARQ) contained in SEQ ID No 2 are not in the sequence, which is present in the database (ACC.: NP 198009.1). NP 198009.1). Compared to version 2 of the database sequence (Acc.: NP 198009.2) the amino acid sequence shown in SEQ ID NO 2 contains the additional amino acids 519 to 523 (WRLCE).

Please amend the paragraph on page 91, lines 15-23, as follows:

The nucleic acid sequence shown in SEQ ID NO 9 codes for a part of an OK1 protein from barley and was traced under "Accession" No.: TC117610 in the TIGR (~~http://~~tigrblast.tigr.org/tgi/) database by means of a database comparison (blast search). Those peptides which were obtained by sequencing the OK1 protein isolated from barley using Q-TOF-MS-MS and were used to identify the EST nucleic acid sequence shown under SEQ ID NO 9, are specified in SEQ ID NO 6, SEQ ID NO 7 and SEQ ID NO 8. The amino acid sequence shown in SEQ ID NO 10 codes for a part of an OK1 protein from barley and can be derived from the nucleic acid sequence shown in SEQ ID NO 10.

Please amend the paragraph on page 91, lines 25-30, to page 92, lines 1-3, as follows:

The nucleic acid sequence shown in SEQ ID NO 15 codes for a part of an OK1 protein from potato and was found under "Accession" No.: BF054632 in the TIGR (~~http://~~tigrblast.tigr.org/tgi/) database by means of a database comparison (blast search). Those peptides which were obtained by sequencing the OK1 protein isolated from potato using Q-TOF-MS-MS and were used to identify the EST nucleic acid sequence shown under SEQ ID NO 15, are specified in SEQ ID NO 11, SEQ ID NO 12, SEQ ID NO 13 and SEQ ID NO 14. The amino acid sequence shown in SEQ ID NO 16 codes for a part of an OK1 protein from potato and can be derived from the nucleic acid sequence shown in SEQ ID NO 15.

Please amend the paragraph on page 92, lines 5 to 13, as follows:

The nucleic acid sequence shown in SEQ ID NO 21 codes for a part of an OK1 protein from millet and was found under "Accession" No.: TC77219 in the TIGR (~~http://~~tigrblast.tigr.org/tgi/) database by means of a database comparison (blast search). Those peptides which were obtained by sequencing the OK1 protein isolated from millet using Q-TOF-MS-MS and were used to identify the EST nucleic acid sequence shown under SEQ ID NO 21, are specified in SEQ ID NO 17, SEQ ID NO 18, SEQ ID NO 19 and SEQ ID NO 20. The amino acid sequence shown in SEQ ID NO 22 codes for a part of an OK1 protein from millet and can be derived from the nucleic acid sequence shown in SEQ ID NO 21.

Please amend the paragraph on page 92, lines 15-29 to page 93, line 1, as follows:

to read as follows:

The nucleic acid sequence shown in SEQ ID NO 25 codes for a part of an OK1 protein from wheat and was found under "Accession" No.: CA74319 in the TIGR (~~http://~~tigrblast.tigr.org/tgi) database by means of a database comparison (blast search). Those peptides which were obtained by sequencing the OK1 protein isolated from wheat using Q-TOF-MS-MS and were used to identify the EST nucleic acid sequence shown under SEQ ID NO 25, are specified in SEQ ID NO 23 and SEQ ID NO 24. The amino acid sequence shown in SEQ ID NO 26 codes for a part of an OK1 protein from wheat and can be derived from the nucleic acid sequence shown in SEQ ID NO 25. The following settings were selected to carry out the database comparisons:

Program:	tblastn
Matrix:	blosum62
Expect:	100
Echofilter:	disabled
Descriptions:	20

All other settings read "default".

Please amend the paragraph on page 99, lines 10-20, as follows:

A. 14. Analysis of Arabidopsis thalliana plants which exhibit a reduced activity of a protein according to the invention

T-DNA insertion mutants of Arabidopsis thaliana (available from the Salk Institute Genomic Analysis Laboratory, 10010 N. Torrey Pines Road, La Jolla, CA 92037, ~~http://~~signal.salk.edu/ under ACC. No.: Salk_110814, Alias N610814), which were homozygotic with respect to insertion in the OK1 gene, were grown under the following conditions:

Light phase: 16 hours, 20°C

Dark phase: 8 hours, 16°C

Shortly before the flowers developed, the plants were cultivated in a light phase of 12 hours at 20°C and a dark phase of 12 hours at 17°C.